BRIGHAM AND WOMEN'S HOSPITAL

HARVARD MEDICAL SCHOOL

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Department of Medicine
Channing Division of Network Medicine

Channing Microbiome Seminar

June 23 (Friday), 2023, 9AM (ET)

MCP 5th-floor large conference room

Zoom: https://us02web.zoom.us/j/81070959105?pwd=RFJNd3dSZmR6dXJZNjJiYVVzQ3NEQT09

Meeting ID: 810 7095 9105

Passcode: 984617

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Phylogenetic Tree-based Microbiome Association Test for Composition Bias

The effects of microbiota on the host phenotypes can substantially differ depending on his/her age. Longitudinally measured microbiome data allows us to detect the age modification effect and are useful for the detection of microorganisms related to the progression of disease which change identification over time. Moreover, longitudinal analysis enables the estimation of within-subject covariate effect, is robust against the between-subject confounders, and provides better evidence for the causal relationship than cross-sectional studies. However, they suffer from compositional bias, and few statistical methods can estimate their effect on host diseases with repeatedly measured 16S rRNA gene data. In this article, we proposed mTMAT which can be applied to longitudinal microbiome data and is robust against compositional bias. mTMAT normalized the microbial abundance and utilized the ratio of the pooled abundances for association analysis. mTMAT is based on generalized estimating equations with a robust variance estimator and can be applied to repeatedly measured microbiome data. With extensive simulation studies, we showed that mTMAT is statistically more powerful and is robust against compositional bias. mTMAT enables detection of microbial taxa associated with host diseases using repeatedly measured 16S rRNA gene data and can provide deeper insight into bacterial pathology.

Bio: Kangjin Kim is a biostatistics and bioinformatics researcher with a strong background in statistics and genetic and metagenomic data analysis. He holds a Doctor of Public Health degree from Seoul National University and currently works as a Postdoctoral Researcher at Brigham Women's Hospital and Harvard Medical School. His research experience includes analyzing large-scale genetic and metagenomics datasets, developing statistical methods, and contributing to projects on pulmonary and metabolic diseases.

Hosted by Yang-Yu Liu